AMIT: A high performance segmentation and tracking framework for migration and confrontation assays

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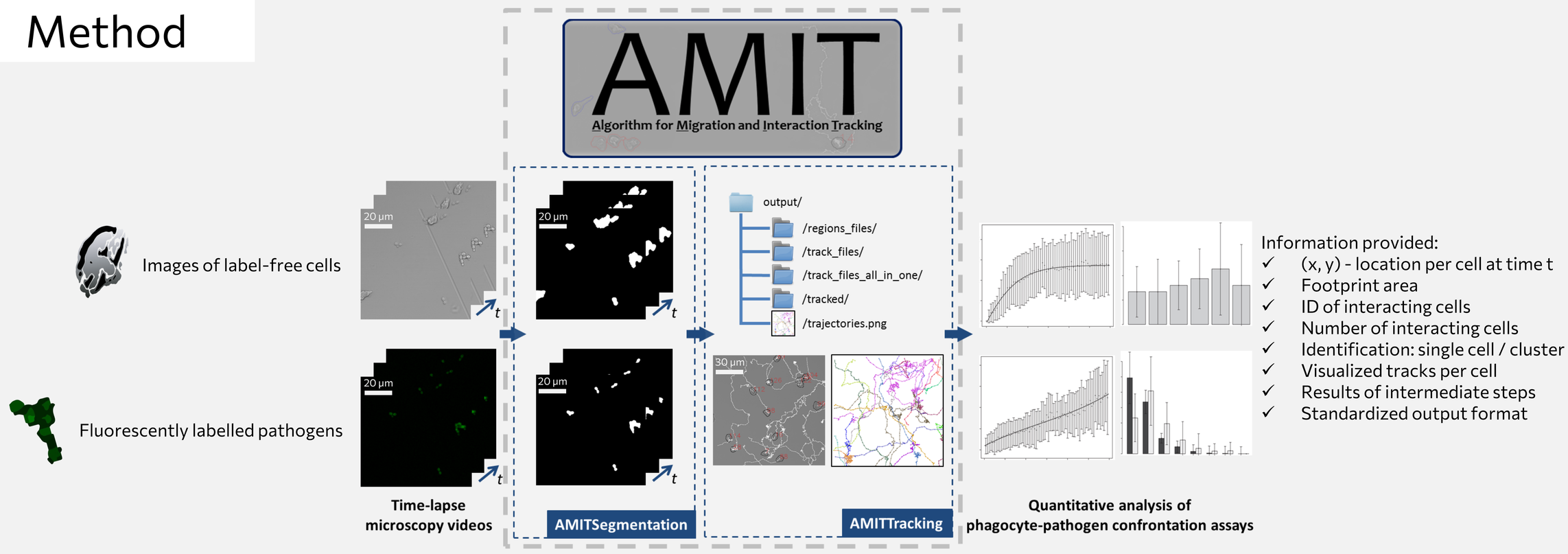
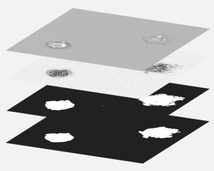
Method



Information provided:
- ✓ (x, y) - location per cell at time t
- ✓ Footprint area
- ✓ ID of interacting cells
- ✓ Number of interacting cells
- ✓ Identification: single cell / cluster
- ✓ Visualized tracks per cell
- ✓ Results of intermediate steps
- ✓ Standardized output format

The algorithm for migration and interaction tracking (AMIT) [1, 2, 3] provides a novel and automated framework for analyzing (label-free) experimental time-lapse microscopy data, in addition to improved detection of whole cell tracks [4]. The approach enables a high throughput processing based on parallelized batch processing through the implementation in the machine-oriented and performant programming language C++, while at the same time detecting nearly all objects in the field of view with high accuracy. The AMIT segmentation method does not rely on any geometric characteristics and can be applied to a wide variety of cell morphologies. The user-friendly application and definition of parameters works via a standardized JSON interface.

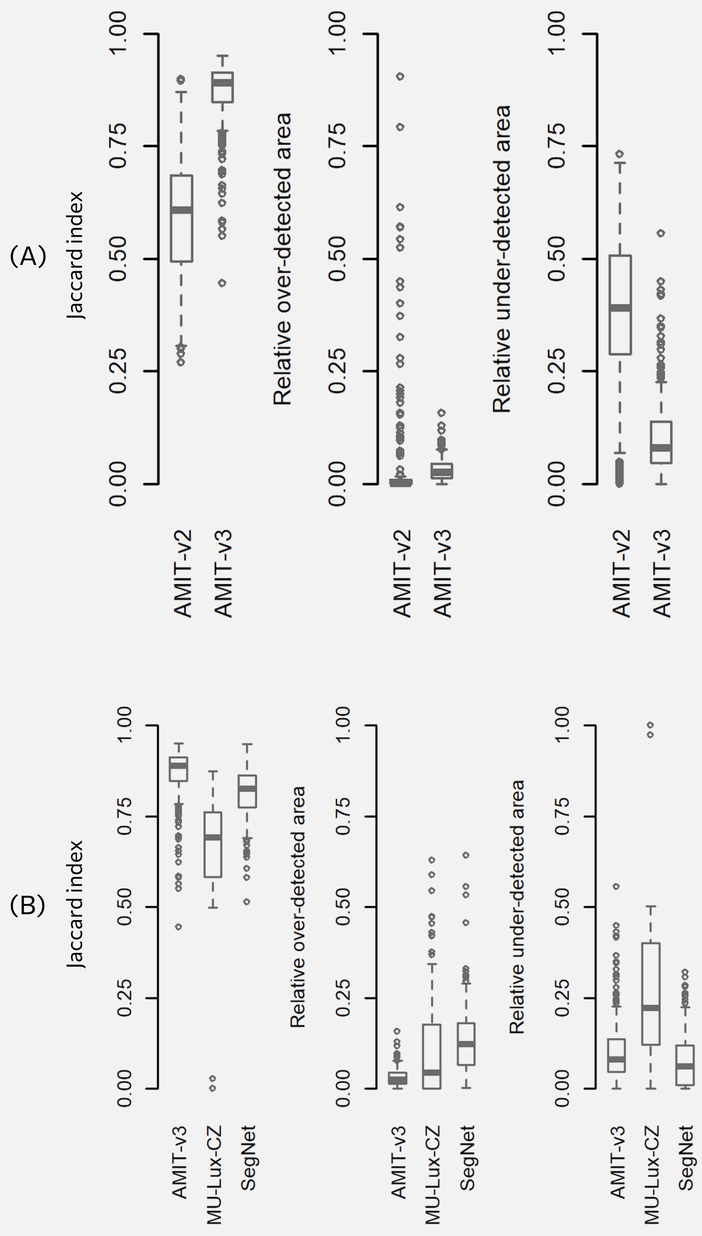
AMITSegmentation is based on
- ➢ Image contrast enhancement using top- and bottom-hat transformation
- ➢ Image denoising by suppression of background variability
- ➢ Enhance high intensity signal by standard deviation filtering
- ➢ Morphology based post-process to suppress artifacts in objects



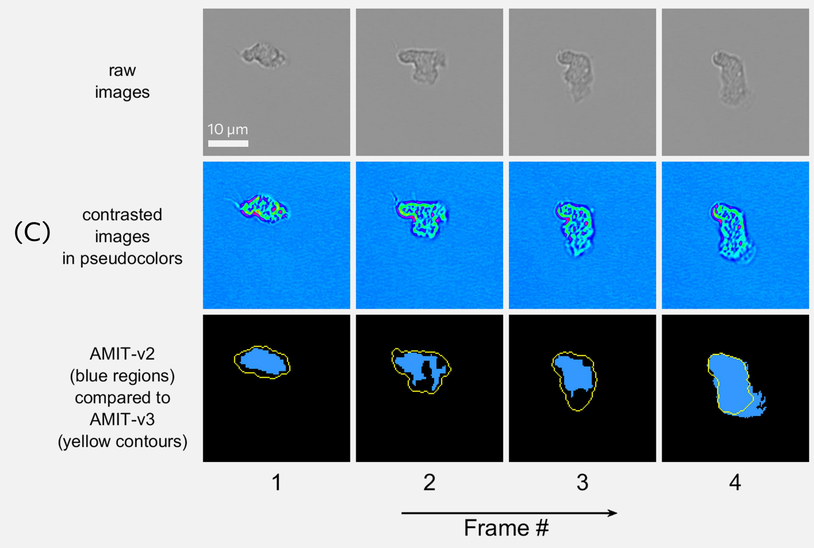
Nearest neighbor based **AMITTracking** connects single cells through
- ➢ Identification of cell clusters by monitoring events of cell-cell fusion and cluster fission
- ➢ Hierarchical cluster splitting based on watershed segmentation

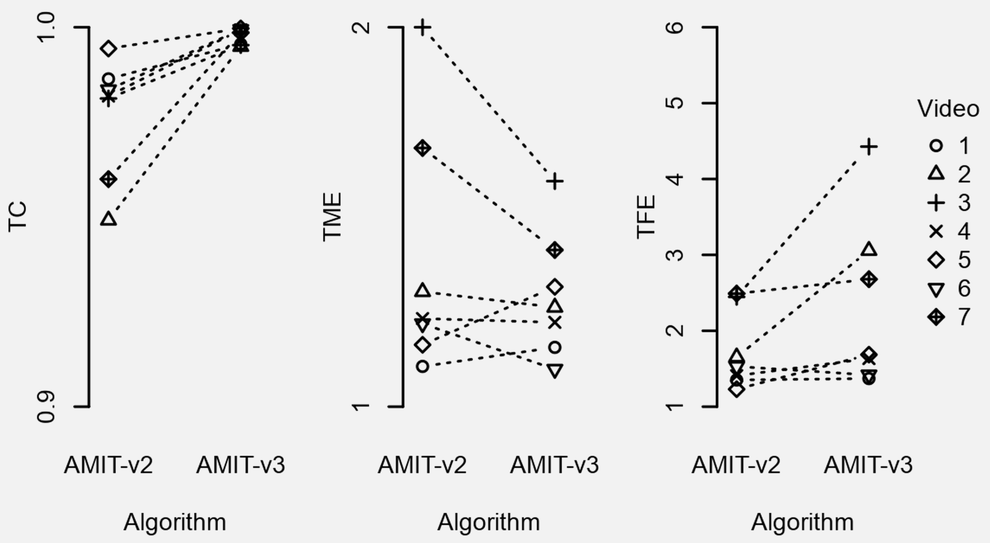
GitHub https://github.com/applied-systems-biology/amit

Performance evaluation



Comparison of the new **Segmentation** (AMIT-v3) with the previous AMIT version (AMIT-v2) [4] (A,C) whereby it becomes clear that the new version detects fewer over- and underdetected areas than the old version. This is visually evident in (C) third row, where AMIT-v3 performs particularly well in low contrast areas, leading to exemplifying visual, as well as quantitative improvement from the new segmentation algorithm.
In addition, we compared AMIT-v3 with deep learning based techniques (B) such as the SegNet [5] and MU-Lux-CZ [6], which require much more time-consuming data preparation, such as creating manual annotation. Again, AMIT-v3 performed the best results overall in terms of an accurate segmentation (see Jaccard index)





Tracking of AMIT-v3 was also compared with AMIT-v2 [4]. The new tracking achieved significantly better results with regard to the total coverage (TC) of all cells. We could also reduce the track merging error (TME) and provide comparable results in terms of the track fragmentation error (TFE).

Summary

AMIT-v3 includes:
- ✓ Accurate segmentation on low contrast cells
- ✓ Tracking of (un)labelled cells in 2D image data
- ✓ Enables analysis of cell cluster (splitting)
- ✓ Analysis of migration / confrontation assays
- ✓ Does not require manual annotations
- ✓ Fast applicability to few image data
- ✓ Parameters are interactively adjustable
- ✓ Accelerated computation times
- ✓ Analysis of high-resolution images on laptops
- ✓ State-of-the-art parallelization
- ✓ Open source availability for everyone

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References
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[3] Brandes *et al.* 2015. *Med Image Anal.* 20(1): 34-51
[4] Al-Zaben *et al.* 2019. *Sci Rep.* 9: 3317
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[6] Lux and Matula. *arXiv.*2004.01607v1.